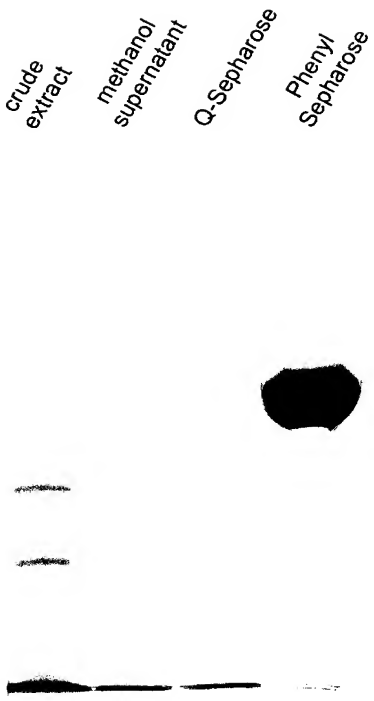
crude extract
methanol supernatant
Q-Sepharose
Phenyl Sepharose

FIG. 1

```
  1 YQQLLQIPAS SPSIFFQDKP FTPDHRDPYD HKVDAIGEGH EPLPWRMGDG  50
 51 ATIMGPRNKD RERQNPDMLR PPSTDHGNMP NMRWSFADSH IRIEEGGWTR 100
101 QTTVRELPTS RELAGVNMRL DEGVIRELHW HREAEWAYVL AGRVRVTGLD 150
151 LEGGSFIDDL EEGDLWYFPS GHPHSLQGLS PNGTEFLLIF DDGNFSEEST 200
201 FLLTDWIAHT PKSVLAGNFR MRPQTFKNIP PSEKYIFQGS VPDSIPKELP 250
251 RNFKASKQRF THKMLAQEPE HTSGGEVRIT DSSNFPISKT VAAAHLTINP 299
300 GAIREMHWHP NADEWSYFKR GRARVTIFAA EGNARTFDYV AGDVGIVPRN 349
350 MGHFIENLSD DEEVEVLEIF RADRFRDFSL FQWMGETPQR MVAEHVFKDD 399
400 PDAAREFLKS VESGEKDPIR SPSE                             424
```

FIG. 2

```
    71                                                                  130
genomic  TTACCAGCAA CTACTGCAGA TTCCCGCCTC ATCCCCATCC ATTTTCTTCC AAGACAAGCC
cDNA     TTACCAGCAA CTACTGCAGA TTCCCGCCTC ATCCCCATCC ATTTTCTTCC AAGACAAGCC
         1                                                                60

       131                                                               190
genomic  ATTCACCCCC GATCATCGCG ACCCCTATGA TCACAAGGTG GATGCGATCG GGGAAGGCCA
cDNA     ATTCACCCCC GATCATCGCG ACCCCTATGA TCACAAGGTG GATGCGATCG GGGAAGGCCA
        61                                                               120

       191                                                               250
genomic  TGAGCCCTTG CCCTGGCGCA TGGGAGATGG AGCCACCATC ATGGGACCCC GCAACAAGGA
cDNA     TGAGCCCTTG CCCTGGCGCA TGGGAGATGG AGCCACCATC ATGGGACCCC GCAACAAGGA
       121                                                               180

       251                                                               310
genomic  CCGTGAGCGC CAGAACCCCG ACATGCTCCG TCCTCCGAGC ACCGACCATG GCAACATGCC
cDNA     CCGTGAGCGC CAGAACCCCG ACATGCTCCG TCCTCCGAGC ACCGACCATG GCAACATGCC
       181                                                               240

       311                                                               370
genomic  GAACATGCGG TGGAGCTTTG CTGACTCCCA CATTCGCATT GAGGTAAGCC CTTCGAGAGT
cDNA     GAACATGCGG TGGAGCTTTG CTGACTCCCA CATTCGCATT GAG..... ..........
       241                                                 283

       371                                                               430
genomic  CTTGTGTACG ACAAGCAAAA TAGGCTAATG CACTGCAGGA GGGCGGCTGG ACACGCCAGA
cDNA     .......... .......... .......... ........GA GGGCGGCTGG ACACGCCAGA
                                           284                     305

       431                                                               490
genomic  CTACCGTACG CGAGCTGCCA ACAAGCAGGG AGCTTGCTGG AGTAAACATG CGCCTTGATG
cDNA     CTACCGTACG CGAGCTGCCA ACAAGCAAGG AGCTTGCTGG AGTAAACATG CGCCTTGATG
       306                                                               365

       491                                                               550
genomic  AGGGTGTCAT TCGCGAGCTG CACTGGCATC GGGAAGCAGA GTGGGCGTAT GTGCTGGCCG
cDNA     AGGGTGTCAT TCGCGAGCTG CACTGGCATC GGGAAGCAGA GTGGGCGTAT GTGCTGGCCG
       366                                                               425

       551                                                               610
genomic  GACGTGTACG AGTGACTGGT CTTGACCTGG AGGGAGGCAG CTTCATCGAT GACCTGGAAG
cDNA     GACGTGTACG AGTGACTGGT CTTGACCTGG AGGGAGGCAG CTTCATCGAT GACCTGGAAG
       426                                                               485
```

FIG. 3A

```
       611                                                                670
genomic  AGGGTGACCT CTGGTACTTC CCATCGGGCC ATCCCCATTC ACTTCAGGGT CTCAGTCCTA
cDNA     AGGGTGACCT CTGGTACTTC CCATCGGGCC ATCCCCATTC ACTTCAGGGT CTCAGTCCTA
       486                                                                545

       671                                                                730
genomic  ATGGCACCGA GTTCTTACTG ATCTTCGACG ATGGAAACTT TTCCGAGGAG TCAACGTTCT
cDNA     ATGGCACCGA GTTCTTACTG ATCTTCGACG ATGGAAACTT TTCCGAGGAG TCAACGTTCT
       546                                                                605

       731                                                                790
genomic  TGTTGACCGA CTGGATCGGT ATGTCCATCA CTATGCTGTT GTACAACCTC CACAAAAATA
cDNA     TGTTGACCGA CTGGATCG.. .......... .......... .......... ..........
       606                 623

       791                                                                850
genomic  CTAACAATGC TATAAAACAG CACATACACC CAAGTCTGTC CTCGCCGGAA ACTTCCGCAT
cDNA     .......... .......... CACATACACC CAAGTCTGTC CTCGCCGGAA ACTTCCGCAT
                          624                                             663

       851                                                                910
genomic  GCGCCCACAA ACATTCAAGA ACATCCCACC ATCTGAAAAG TACATCTTCC AGGGCTCTGT
cDNA     GCGCCCACAA ACATTCAAGA ACATCCCACC ATCTGAAAAG TACATCTTCC AGGGCTCTGT
       664                                                                723

       911                                                                970
genomic  CCCAGACTCT ATCCCCAAAG AACTTCCCCG CAACTTCAAA GCATCCAAGC AGCGCTTCAC
cDNA     CCCAGACTCT ATCCCCAAAG AACTTCCCCG CAACTTCAAA GCATCCAAGC AGCGCTTCAC
       724                                                                783

       971                                                               1030
genomic  GCATAAGATG CTCGCTCAAG AACCCGAGCA TACCTCTGGC GGAGAGGTGC GCATCACAGA
cDNA     GCATAAGATG CTCGCTCAAG AACCCGAGCA TACCTCTGGC GGAGAGGTGC GCATCACAGA
       784                                                                843

      1031                                                               1090
genomic  CTCGTCCAAC TTTCCCATCT CCAAGACGGT CGCGGCCGCC CACCTGACCA TTAACCCGGG
cDNA     CTCGTCCAAC TTTCCCATCT CCAAGACGGT CGCGGCCGCC CACCTGACCA TTAACCCGGG
       844                                                                903

      1091                                                               1150
genomic  CGCTATCCGG GAGATGCACT GGCATCCCAA TGCGGATGAA TGGTCCTACT TTAAGCGCGG
cDNA     CGCTATCCGG GAGATGCACT GGCATCCCAA TGCGGATGAA TGGTCCTACT TTAAGCGCGG
       904                                                                963

      1151                                                               1210
genomic  TCGGGCGCGA GTGACTATCT TCGCTGCTGA AGGTAATGCT CGTACATTCG ACTACGTAGC
cDNA     TCGGGCGCGA GTGACTATCT TCGCTGCTGA AGGTAATGCT CGTACATTCG ACTACGTAGC
       964                                                               1023
```

FIG. 3B

```
      1211                                                                1270
genomic  GGGAGATGTG GGCATTGTTC CTCGCAACAT GGGTCATTTC ATTGAGAACC TCAGTGATGA
cDNA     GGGAGATGTG GGCATTGTTC CTCGCAACAT GGGTCATTTC ATTGAGAACC TCAGTGATGA
      1024                                                                1083

      1271                                                                1330
genomic  CGAGGAGGTC GAGGTGTTGG AAATCTTCCG GGCGGACCGA TTCCGGGACT TTTCGTTGTT
cDNA     CGAGGAGGTC GAGGTGTTGG AAATCTTCCG GGCGGACCGA TTCCGGGACT TTTCGTTGTT
      1084                                                                1143

      1331                                                                1390
genomic  CCAGTGGATG GGAGAGACGC CGCAGCGGAT GGTGGCAGAG CATGTGTTTA AGGATGATCC
cDNA     CCAGTGGATG GGAGAGACGC CGCAGCGGAT GGTGGCAGAG CATGTGTTTA AGGATGATCC
      1144                                                                1203

      1391                                                                1450
genomic  AGATGCGGCC AGGGAGTTCC TTAAGAGTGT GGAGAGCGGG GAGAAGGATC CAATTCGGAG
cDNA     AGATGCGGCC AGGGAGTTCC TTAAGAGTGT GGAGAGCGGG GAGAAGGATC CGATTCGGAG
      1204                                                                1263

      1451                1467
genomic  CCCAAGTGAG TAGATGA
cDNA     CCCAAGTGAG TAGATGA
      1264                1280
```

FIG. 3C

CTATGCATCC AACGCGTTGG GAGCTCTCCC ATATGGTCGA CCTGCAGGCG GCCGCGAATT CACTAGTGAT
TTACCAGCAA CTACTGCAGA TTCCCGCCTC ATCCCCATCC ATTTTCTTCC AAGACAAGCC ATTCACCCCC
GATCATCGCG ACCCCTATGA TCACAAGGTG GATGCGATCG GGGAAGGCCA TGAGCCCTTG CCCTGGCGCA
TGGGAGATGG AGCCACCATC ATGGGACCCC GCAACAAGGA CCGTGAGCGC CAGAACCCCG ACATGCTCCG
TCCTCCGAGC ACCGACCATG GCAACATGCC GAACATGCGG TGGAGCTTTG CTGACTCCCA CATTCGCATT
GAGGTAAGCC CTTCGAGAGT CTTGTGTACG ACAAGCAAAA TAGGCTAATG CACTGCAGGA GGGCGGCTGG
ACACGCCAGA CTACCGTACG CGAGCTGCCA ACAAGCAGGG AGCTTGCTGG AGTAAACATG CGCCTTGATG
AGGGTGTCAT TCGCGAGCTG CACTGGCATC GGGAAGCAGA GTGGGCGTAT GTGCTGGCCG GACGTGTACG
AGTGACTGGT CTTGACCTGG AGGGAGGCAG CTTCATCGAT GACCTGGAAG AGGGTGACCT CTGGTACTTC
CCATCGGGCC ATCCCCATTC ACTTCAGGGT CTCAGTCCTA ATGGCACCGA GTTCTTACTG ATCTTCGACG
ATGGAAACTT TTCCGAGGAG TCAACGTTCT TGTTGACCGA CTGGATCGGT ATGTCCATCA CTATGCTGTT
GTACAACCTC CACAAAAATA CTAACAATGC TATAAAACAG CACATACACC CAAGTCTGTC CTCGCCGGAA
ACTTCCGCAT GCGCCCACAA ACATTCAAGA ACATCCCACC ATCTGAAAAG TACATCTTCC AGGGCTCTGT
CCCAGACTCT ATCCCCAAAG AACTTCCCCG CAACTTCAAA GCATCCAAGC AGCGCTTCAC GCATAAGATG
CTCGCTCAAG AACCCGAGCA TACCTCTGGC GGAGAGGTGC GCATCACAGA CTCGTCCAAC TTTCCCATCT
CCAAGACGGT CGCGGCCGCC CACCTGACCA TTAACCCGGG CGCTATCCGG GAGATGCACT GGCATCCCAA
TGCGGATGAA TGGTCCTACT TTAAGCGCGG TCGGGCGCGA GTGACTATCT TCGCTGCTGA AGGTAATGCT
CGTACATTCG ACTACGTAGC GGGAGATGTG GGCATTGTTC CTCGCAACAT GGGTCATTTC ATTGAGAACC
TCAGTGATGA CGAGGAGGTC GAGGTGTTGG AAATCTTCCG GGCGGACCGA TTCCGGGACT TTTCGTTGTT
CCAGTGGATG GGAGAGACGC CGCAGCGGAT GGTGGCAGAG CATGTGTTTA AGGATGATCC AGATGCGGCC
AGGGAGTTCC TTAAGAGTGT GGAGAGCGGG GAGAAGGATC CAATTCGGAG CCCAAGTGAG TAGATGAAAT
CGAATTCCCG CGGCCGCCAT GGCGGCCGGG AGCATGCGAC GT (1512)

FIG. 4

```
  1 MKKQNDIPQP IRGDKGATVK IPRNIERDRQ NPDMLVPPET DHGTVSNMKF  50
 51 SFSDTHNRLE KGGYAREVTV RELPISENLA SVNMRLKPGA IRELHWHKEA 100
101 EWAYMIYGSA RVTIVDEKGR SFIDDVGEGD LWYFPSGLPH SIQALEEGAE 151
151 FLLVFDDGSF SENSTFQLTD WLAHTPKEVI AANFGVTKEE ISNLPGKEKY 200
201 IFENQLPGSL KDDIVEGPNG EVPYPFTYRL LEQEPIESEG GKVYIADSTN 250
251 FKVSKTIASA LVTVEPGAMR ELHWHPNTHE WQYYISGKAR MTVFASDGHA 299
300 RTFNYQAGDV GYVPFAMGHY VENIGDEPLV FLEIFKDDHY ADVSLNQWLA 349
350 MLPETFVQAH LDLGKDFTDV LSKEKHPVVK KKCSK               385
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FIG. 5